



#9

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/899,569

Source: OTPE

Date Processed by STIC: 7/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

Does Not Comply
Corrected Diskette Needed
see Add 1

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/899,569

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 07/20/2001

PATENT APPLICATION: US/09/899,569

TIME: 14:20:30

Input Set : A:\0652 2280001 seq list.txt

Output Set: N:\CRF3\07202001\I899569.raw

Does Not Comply
Corrected Diskette Needed
See Add 1

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4 <110> APPLICANT: Schweifer, Norbert
5   Scherl-Mostageer, Marwa
6   Sommergruber, Wolfgang
7   Abseher, Roger
9 <120> TITLE OF INVENTION: Tumorassoziertes Antigen (B345)
11 <130> FILE REFERENCE: 0652.2280001/EKS/AES
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/899,569
C--> 14 <141> CURRENT FILING DATE: 2001-07-06
16 <150> PRIOR APPLICATION NUMBER: DE 100 33 080.0
17 <151> PRIOR FILING DATE: 2000-07-07
19 <150> PRIOR APPLICATION NUMBER: DE 101 19 294.0.
20 <151> PRIOR FILING DATE: 2001-04-19
22 <150> PRIOR APPLICATION NUMBER: US 60/243,158
23 <151> PRIOR FILING DATE: 2000-10-25
25 <150> PRIOR APPLICATION NUMBER: US 60/297,747
26 <151> PRIOR FILING DATE: 2001-06-14
28 <160> NUMBER OF SEQ ID NOS: 40
30 <170> SOFTWARE: PatentIn Ver. 2.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 5897
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
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41 <222> LOCATION: (1)..(214)
43 <220> FEATURE:
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45 <222> LOCATION: (215)..(2464)
47 <220> FEATURE:
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56   acgagaaagc aacattacag ttctcataaa gctggggacc ccgactctgc tggcaaaacc 180
58   ctgttacatc gtcatttcta aaagacatat aacc atg ttg tcc atc aag tct gga 235
59                                     Met Leu Ser Ile Lys Ser Gly
60                                     1           5
62   gaa aga ata gtc ttt acc ttt agc tgc cag agt cct gag aat cac ttt   283
63   Glu Arg Ile Val Phe Thr Phe Ser Cys Gln Ser Pro Glu Asn His Phe
64       10           15           20
66   gtc ata gag atc cag aaa aat att gac tgt atg tca ggc cca tgt cct   331
67   Val Ile Glu Ile Gln Lys Asn Ile Asp Cys Met Ser Gly Pro Cys Pro
68       25           30           35
70   ttt ggg gag gtt cag ctt cag ccc tcg aca tcg ttg ttg cct acc ctc   379
71   Phe Gly Glu Val Gln Leu Gln Pro Ser Thr Ser Leu Leu Pro Thr Leu
72   40           45           50           55

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76 Asn Arg Thr Phe Ile Trp Asp Val Lys Ala His Lys Ser Ile Gly Leu
77          60          65          70
79 gag ctg cag ttt tcc atc cct cgc ctg agg cag atc ggt ccg ggt gag 475
80 Glu Leu Gln Phe Ser Ile Pro Arg Leu Arg Gln Ile Gly Pro Gly Glu
81          75          80          85
83 agc tgc cca gac gga gtc act cac tcc atc agc ggc cga atc gat gcc 523
84 Ser Cys Pro Asp Gly Val Thr His Ser Ile Ser Gly Arg Ile Asp Ala
85          90          95          100
87 acc gtg gtc agg atc gga acc ttc tgc agc aat ggc act gtg tcc cgg 571
88 Thr Val Val Arg Ile Gly Thr Phe Cys Ser Asn Gly Thr Val Ser Arg
89          105          110          115
91 atc aag atg caa gaa gga gtg aaa atg gcc tta cac ctc cca tgg ttc 619
92 Ile Lys Met Gln Glu Gly Val Lys Met Ala Leu His Leu Pro Trp Phe
93 120          125          130          135
95 cac ccc aga aat gtc tcc ggc ttc agc att gca aac cgc tca tct ata 667
96 His Pro Arg Asn Val Ser Gly Phe Ser Ile Ala Asn Arg Ser Ser Ile
97          140          145          150
99 aaa cgt ctg tgc atc atc gag tct gtg ttt gag ggt gaa ggc tca gca 715
100 Lys Arg Leu Cys Ile Ile Glu Ser Val Phe Glu Gly Glu Gly Ser Ala
101          155          160          165
103 acc ctg atg tct gcc aac tac cca gaa ggc ttc cct gag gat gag ctc 763
104 Thr Leu Met Ser Ala Asn Tyr Pro Glu Gly Phe Pro Glu Asp Glu Leu
105          170          175          180
107 atg acg tgg cag ttt gtc gtt cct gca cac ctg cgg gcc agc gtc tcc 811
108 Met Thr Trp Gln Phe Val Val Pro Ala His Leu Arg Ala Ser Val Ser
109          185          190          195
111 ttc ctc aac ttc aac ctc tcc aac tgt gag agg aag gag gag cgg gtt 859
112 Phe Leu Asn Phe Asn Leu Ser Asn Cys Glu Arg Lys Glu Glu Arg Val
113 200          205          210          215
115 gaa tac tac atc ccg ggc tcc acc acc aac ccc gag gtg ttc aag ctg 907
116 Glu Tyr Tyr Ile Pro Gly Ser Thr Thr Asn Pro Glu Val Phe Lys Leu
117          220          225          230
119 gag gac aag cag cct ggg aac atg gcg ggg aac ttc aac ctc tct ctg 955
120 Glu Asp Lys Gln Pro Gly Asn Met Ala Gly Asn Phe Asn Leu Ser Leu
121          235          240          245
123 caa ggc tgt gac caa gat gcc caa agt cca ggg atc ctc cgg ctg cag 1003
124 Gln Gly Cys Asp Gln Asp Ala Gln Ser Pro Gly Ile Leu Arg Leu Gln
125          250          255          260
127 ttc caa gtt ttg gtc caa cat cca caa aat gaa agc aat aaa atc tac 1051
128 Phe Gln Val Leu Val Gln His Pro Gln Asn Glu Ser Asn Lys Ile Tyr
129          265          270          275
133 gtg gtt gac ttg agt aat gag cga gcc atg tca ctc acc atc gag cca 1099
134 Val Val Asp Leu Ser Asn Glu Arg Ala Met Ser Leu Thr Ile Glu Pro
135 280          285          290          295
137 cgg ccc gtc aaa cag agc cgc aag ttt gtc cct ggc tgt ttc gtg tgt 1147
138 Arg Pro Val Lys Gln Ser Arg Lys Phe Val Pro Gly Cys Phe Val Cys
139          300          305          310
142 cta gaa tct cgg acc tgc agt agc aac ctc acc ctg aca tct ggc tcc 1195

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143	Leu	Glu	Ser	Arg	Thr	Cys	Ser	Ser	Asn	Leu	Thr	Leu	Thr	Ser	Gly	Ser	
144				315					320					325			
146	aaa	cac	aaa	atc	tcc	ttc	ctt	tgt	gat	gat	ctg	aca	cgt	ctg	tgg	atg	1243
147	Lys	His	Lys	Ile	Ser	Phe	Leu	Cys	Asp	Asp	Leu	Thr	Arg	Leu	Trp	Met	
148			330					335					340				
150	aat	gtg	gaa	aaa	acc	ata	agc	tgc	aca	gac	cac	cgg	tac	tgc	caa	agg	1291
151	Asn	Val	Glu	Lys	Thr	Ile	Ser	Cys	Thr	Asp	His	Arg	Tyr	Cys	Gln	Arg	
152		345					350					355					
154	aaa	tcc	tac	tca	ctc	cag	gtg	ccc	agt	gac	atc	ctc	cac	ctg	cct	gtg	1339
155	Lys	Ser	Tyr	Ser	Leu	Gln	Val	Pro	Ser	Asp	Ile	Leu	His	Leu	Pro	Val	
156	360					365				370					375		
158	gag	ctg	cat	gac	ttc	tcc	tgg	aag	ctg	ctg	gtg	ccc	aag	gac	agg	ctc	1387
159	Glu	Leu	His	Asp	Phe	Ser	Trp	Lys	Leu	Leu	Val	Pro	Lys	Asp	Arg	Leu	
160				380					385					390			
162	agc	ctg	gtg	ctg	gtg	cca	gcc	cag	aag	ctg	cag	cag	cat	aca	cac	gag	1435
163	Ser	Leu	Val	Leu	Val	Pro	Ala	Gln	Lys	Leu	Gln	Gln	His	Thr	His	Glu	
164			395					400					405				
166	aag	ccc	tgc	aac	acc	agc	ttc	agc	tac	ctc	gtg	gcc	agt	gcc	ata	ccc	1483
167	Lys	Pro	Cys	Asn	Thr	Ser	Phe	Ser	Tyr	Leu	Val	Ala	Ser	Ala	Ile	Pro	
168			410				415					420					
170	agc	cag	gac	ctg	tac	ttc	ggc	tcc	ttc	tgc	ccg	gga	ggc	tct	atc	aag	1531
171	Ser	Gln	Asp	Leu	Tyr	Phe	Gly	Ser	Phe	Cys	Pro	Gly	Gly	Ser	Ile	Lys	
172		425				430				435							
174	cag	atc	cag	gtg	aag	cag	aac	atc	tcg	gtg	acc	ctt	cgc	acc	ttt	gcc	1579
175	Gln	Ile	Gln	Val	Lys	Gln	Asn	Ile	Ser	Val	Thr	Leu	Arg	Thr	Phe	Ala	
176	440				445				450						455		
178	ccc	agc	ttc	caa	caa	gag	gcc	tcc	agg	cag	ggt	ctg	acg	gtg	tcc	ttt	1627
179	Pro	Ser	Phe	Gln	Gln	Ala	Ser	Arg	Gln	Gly	Leu	Thr	Val	Ser	Phe		
180			460				465					470					
182	ata	cct	tat	ttc	aaa	gag	gaa	ggc	gtt	ttc	acg	gtg	acc	cct	gac	aca	1675
183	Ile	Pro	Tyr	Phe	Lys	Glu	Glu	Gly	Val	Phe	Thr	Val	Thr	Pro	Asp	Thr	
184			475				480					485					
186	aaa	agc	aag	gtc	tac	ctg	agg	acc	ccc	aac	tgg	gac	cgg	ggc	ctg	cca	1723
187	Lys	Ser	Lys	Val	Tyr	Leu	Arg	Thr	Pro	Asn	Trp	Asp	Arg	Gly	Leu	Pro	
188			490				495				500						
191	tcc	ctc	acc	tct	gtg	tcc	tgg	aac	atc	agc	gtg	ccc	aga	gac	cag	gtg	1771
192	Ser	Leu	Thr	Ser	Val	Ser	Trp	Asn	Ile	Ser	Val	Pro	Arg	Asp	Gln	Val	
193		505				510					515						
195	gcc	tgc	ctg	act	ttc	ttt	aag	gag	cgg	agc	ggc	gtg	gtc	tgc	cag	aca	1819
196	Ala	Cys	Leu	Thr	Phe	Phe	Lys	Glu	Arg	Ser	Gly	Val	Val	Cys	Gln	Thr	
197	520				525				530					535			
199	ggg	cgc	gca	ttc	atg	atc	atc	cag	gag	cag	cgg	acc	cgg	gct	gag	gag	1867
200	Gly	Arg	Ala	Phe	Met	Ile	Ile	Gln	Glu	Gln	Arg	Thr	Arg	Ala	Glu	Glu	
201			540				545							550			
203	atc	ttc	agc	ctg	gac	gag	gat	gtg	ctc	ccc	aag	cca	agc	ttc	cac	cat	1915
204	Ile	Phe	Ser	Leu	Asp	Glu	Asp	Val	Leu	Pro	Lys	Pro	Ser	Phe	His	His	
205			555				560					565					
207	cac	agc	ttc	tgg	gtc	aac	atc	tct	aac	tgc	agc	ccc	acg	agc	ggc	aag	1963
208	His	Ser	Phe	Trp	Val	Asn	Ile	Ser	Asn	Cys	Ser	Pro	Thr	Ser	Gly	Lys	

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213          585          590          595
215  ttg act gtc atc ctc atc gca gcg gtg gga ggt gga gtc tta ctg ctg 2059
216  Leu Thr Val Ile Leu Ile Ala Ala Val Gly Gly Gly Val Leu Leu Leu
217  600          605          610          615
219  tct gcc ctc ggg ctc atc att tgc tgt gtg aaa aag aag aaa aag aag 2107
220  Ser Ala Leu Gly Leu Ile Ile Cys Cys Val Lys Lys Lys Lys Lys Lys
221          620          625          630
223  aca aac aag ggc ccc gct gtg ggt atc tac aat ggc aac atc aat act 2155
224  Thr Asn Lys Gly Pro Ala Val Gly Ile Tyr Asn Gly Asn Ile Asn Thr
225          635          640          645
227  gag atg cca ggc agc caa aaa agt ttc aga aag ggc gaa agg aca atg 2203
228  Glu Met Pro Gly Ser Gln Lys Ser Phe Arg Lys Gly Glu Arg Thr Met
229          650          655          660
231  act ccc atg tgt atg cag tca tcg agg aca cca tgg tat atg ggc atc 2251
232  Thr Pro Met Cys Met Gln Ser Ser Arg Thr Pro Trp Tyr Met Gly Ile
233          665          670          675
235  tgc tac agg att cca gcg gct cct tcc tgc agc cag agg tgg aca cct 2299
236  Cys Tyr Arg Ile Pro Ala Ala Pro Ser Cys Ser Gln Arg Trp Thr Pro
237  680          685          690          695
239  acc ggc cgt tcc agg gca cca tgg ggg tct gtc ctc cct ccc cac cca 2347
240  Thr Gly Arg Ser Arg Ala Pro Trp Gly Ser Val Leu Pro Pro His Pro
241          700          705          710
243  cca tat gct cca ggg ccc caa ctg caa agt tgg cca ctg agg agc cac 2395
244  Pro Tyr Ala Pro Gly Pro Gln Leu Gln Ser Trp Pro Leu Arg Ser His
245          715          720          725
249  ctc ctc gct ccc ctc ctg agt ctg aga gtg aac cgt aca cct tct ccc 2443
250  Leu Leu Ala Pro Leu Leu Ser Leu Arg Val Asn Arg Thr Pro Ser Pro
251          730          735          740
253  atc cca aca atg ggg atg taa gcagcaagga cacagacatt cccttactga 2494
254  Ile Pro Thr Met Gly Met
W--> 255          745          750 ————— remove
257  acactcagga gcccatggag ccagcagaat aacttgatcc attccagacg ctttgcctgag 2554
259  tttcataaag cagggcactg agacacccgt ccgtgttcct aaccagaaat cctaaagaag 2614
261  aggaattata cagaaggaac agcaggaggt tttcctggac accgccaact tcacattgct 2674
263  cagtggactc attctaaggg caagacattg aaaatgatga attccaatct ggatacagtc 2734
265  atgacagctc atgtgtcctt caacttaggc tgtgcggtta gccagcctgt aatgagagga 2794
267  gagaggcctg agtcacctag catagggttg cagcaagccc tggattcaga gtgttaaaca 2854
269  gaggettgcg ctcttcagga caacagttcc aattccaagg agcctacctg aggtccctac 2914
271  tctcaactgg gtccccagga tgaaaacgac aatgtgcctt tttattatta tttatttggt 2974
273  ggtcctgtgt tatttaagag atcaaatgta taaccaccta gctcttttca cctgacttag 3034
275  taataactca tactaactgg tttggatgcc tgggttgga cttctactga ccgctagata 3094
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281  aggtcggttc gtggttatcc cattgtggaa attcatcttg aatcccattg tcctatagtc 3274
283  ctagcaataa gagaaatttc ctcaagtttc catgtgcggt tctcctagct gcagcaatac 3334
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289 ttaaaaacaa cacattagct tatagtcctg gggatcagaa ttccaaaatg gatgtccctg 3514
291 aatgaaaatc aaggtgtcag cagagctgtg ctcccttctga aggcctctagg gagaagcccg 3574
293 ttcccttgcca tttcaagctt ctagaggctg gctgcattcc caggctccag tggctggtca 3634
295 agctttttctc acatggcatc actgtgacac tggccctccc acttccctct ttgacttaca 3694
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325 cccacaccct catttatacc aattacctgc ccagtaactg tggacttttg cttcctcacc 4594
327 cctgctctga tctggaagga gagggattat gttatagctt gtcagcacag tcccaagttc 4654
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331 ttcaccttgg aaatgcaccg cctcaacttg ttcacatggc ataaatgaaa ggaattttat 4774
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337 cagtgaacct tggccttgtg agccgagatg ctgacctgac ataaagggcc aaaggagggc 4954
339 tgcggcttcc ttcctcact gaagagccct tatttgaatt cactgtgtgg agccctagcc 5014
341 ctccattctc gacattcccc aacctcccag ccccttccaa gcaggactag gtgccctgca 5074
343 tccaccccaa ggtgggattg gccttcccta ggtctgttac ttgtcaccat caccgacatc 5134
345 actgttgctt gcaaggacac cacgtggcca ttttccctca actgagggtt caaaactcct 5194
347 ggacaagtgt ctggctcctg agaccagtat ttcctggagm tgtgcctcag tgaagggggc 5254
349 cagcctgagg aacctggtt cttttcttta aagcccaggc cccacttaca taaaacattt 5314
W--> 351 cagggctcact ggaaacagtg aagtgccatt tgttgaagcc tactgmatgc cagcccactg 5374
W--> 353 ctcatccacg tggtagcca tgcctacgag gaaggccagc gcatgcagga atgggtctcta 5434
W--> 355 atgtgtggt cattgcacag aagggaaagg tctcaaggaa gactcaactg ggacaagcac 5494
357 aagcccaccg gacatggcct tggtaaaggt tagcagactg gtgtgtgtgg atctgcagtg 5554
359 cttcactgga aataatttat tcattgcaga tacttttttag gtggcatttt attcatttcc 5614
361 tgtgctttta ataaacaaat gtacaaaaaa acaagtatca agctgtttta gtgcttcggc 5674
363 tacttgctcc ctggttcagt agaggccccg gtttccctagt tgttgactgt gacaggctca 5734
365 gcatgggctc agcagatgct gtcttaattt gtggatgata cagaaagcca ggctttggga 5794
367 tacaagttct ttcctcttca tttgatgccg tgcactgtgt gaagcagatg tttttgtccg 5854
369 gaaataaaaa taatagtctt ggagtctcgc caaaaaaaa aag 5897
373 <210> SEQ ID NO: 2
374 <211> LENGTH: 749
375 <212> TYPE: PRT
376 <213> ORGANISM: Homo sapiens
378 <400> SEQUENCE: 2
379 Met Leu Ser Ile Lys Ser Gly Glu Arg Ile Val Phe Thr Phe Ser Cys
380 1 5 10 15

```

See item
number 9 on
Error Summary
Sheet

<210> 38
 <211> 23
 <212> DNA
 <213> Kunstliche Sequenz

<220>
 <221> 5'UTR
 <222> (1) .. (282)

<220>
 <221> GC_signal
 <222> (147) .. (157)

<220>
 <221> misc_feature
 <222> (201) .. (209)
 <223> cap signal; Transkriptionsstart

<220>
 <221> 3'UTR
 <222> (2794) .. (6163)

<220>
 <221> 3'UTR
 <222> (2794) .. (6163)

<220>
 <221> CDS
 <222> (283) .. (2793)

<400> 38
 agcagcagaa cccctagcag tgc

The ranges provided
 for numeric identifier
 <222> are larger than
 the actual sequence.

VERIFICATION SUMMARY

DATE: 07/20/2001

PATENT APPLICATION: US/09/899,569

TIME: 14:20:31

Input Set : A:\0652 2280001 seq list.txt

Output Set: N:\CRF3\07202001\I899569.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:351 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:353 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1500 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 5UTR LOCATION: (1)..
(282)
L:1513 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 3UTR LOCATION:
(2794)..(6163)
L:1517 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, 3UTR LOCATION:
(2794)..(6163)
L:1521 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:38, CDS LOCATION: (283)..
(2793)